

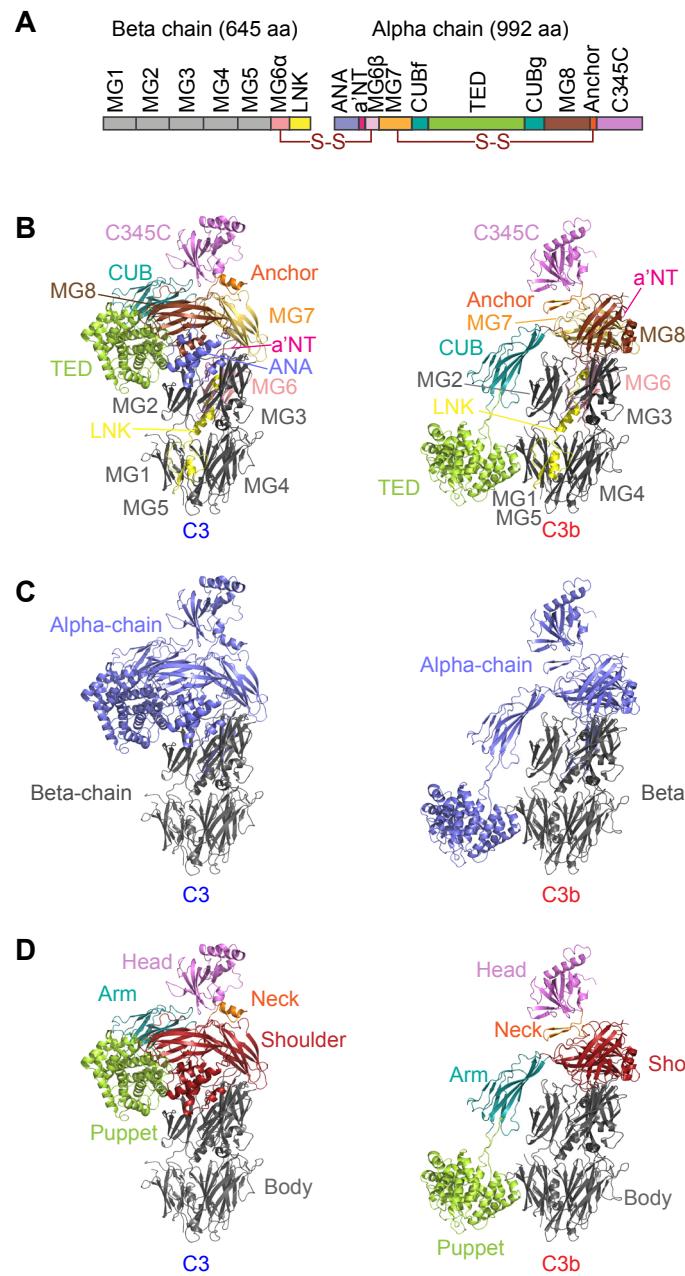
Supplemental Information

Structure of complement C3(H₂O) revealed by quantitative cross-linking/mass spectrometry and modelling

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Supplemental Figure 1

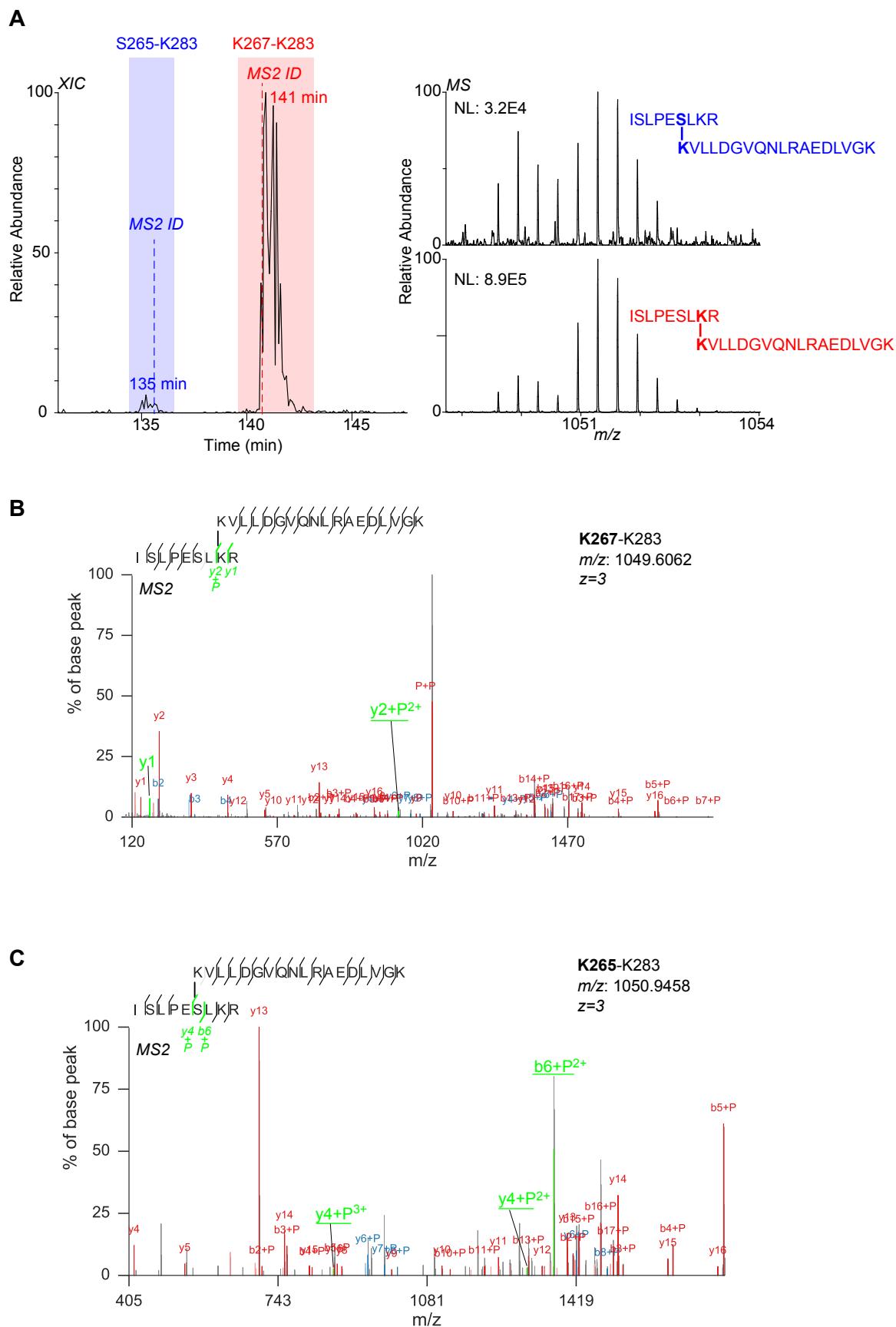


Supplemental Figure 1: Domain arrangements of C3 and C3b in the crystal structures

(A) Summary of the multiple domains of C3 (24). (B) Domains of C3 and C3b are coloured and labelled in the crystal structures of C3 (PDB|2A73) and C3b (PDB|2I07) (the same PDB entries are used for C and D). (C) The α -chain and the β -chain of C3/C3b are coloured and labelled in the crystal structures of C3 and C3b (D) The crystal structures of C3 and C3b are coloured and labelled according to the metaphor of a puppeteer (1).

1. Janssen, B. J., Christodoulidou, A., McCarthy, A., Lambris, J. D., and Gros, P. (2006) Structure of C3b reveals conformational changes that underlie complement activity. *Nature* 444, 213-216

Supplemental Figure S2

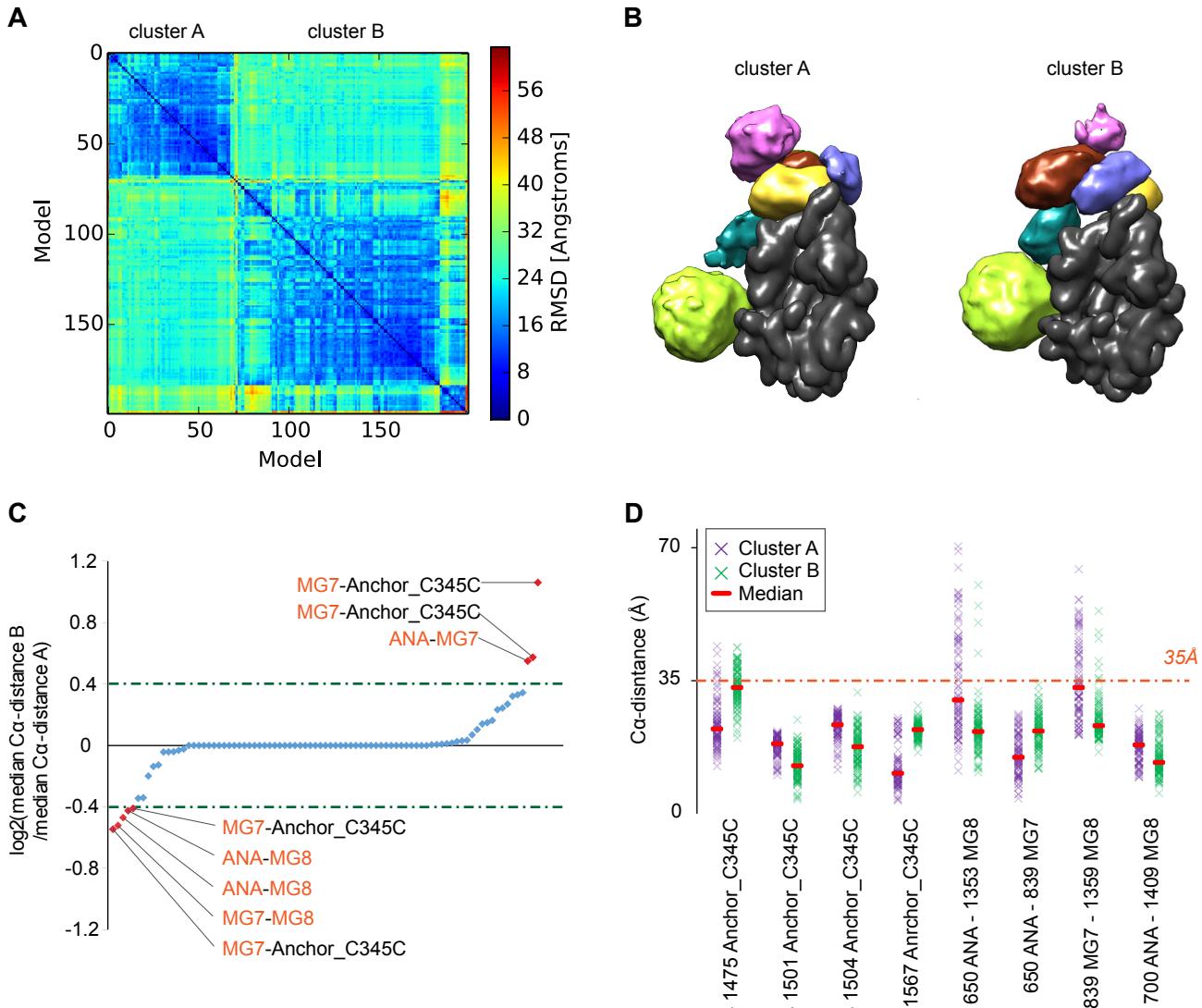


Supplemental Fig S2. Assessment of cross-link site assignment

Assessment of site assignment of cross-linked peptides is demonstrated using an example.

(A) The peptides ISLPESLKR and KVLLDGVQNLRAEDLVGK were found cross-linked in two ways, once linking 267K and 283K and once linking 265S and 283K. The 267K – 283K linked peptide eluted with a retention time of 141 minute from our HPLC system and was assigned this linkage based on back-bone fragments y1 and y2+P ions that flank 267K (annotated spectrum shown in(B)). 265S – 283K is placed in close sequence proximity to 267K – 283K. Given the much higher reactivity of NHS-esters to K when compared to S, special caution needed to be employed when calling 265S – 283K. 265S is supported over 267K in the matching fragmentation spectrum by the observation of b6+P and y4+P ions that flank 265S (annotated spectrum shown in (C)). In addition, the 265S – 283K peptide eluted at 135 minute in a base line separated peak from our HPLC system. Notably, the intensity of this peptide is much lower than that carrying the 267K – 283K link as one might expect considering the reactivity difference of S and K.

Supplemental Figure S3



Supplementary Figure 3. Clustering of C3(H₂O) solutions.

The 200 best scoring models (solutions) were partitioned into clusters, using the k-means clustering method. The two blue blocks of the pair-wise r.m.s.-distance matrix calculated between the 200 models (**A**) suggested the presence of at least two main clusters of similar structures. The resulting clusters (**B**) displayed a different orientation of MG8 (brown density) and ANA (violet density), with respect to the other domains. A comparison of the distances between cross-linked residues, in cluster A *versus* cluster B, is shown in (**C**). For each cross-link (displayed along the x-axis) the ratio (for cluster A *versus* cluster B) of median C α -C α distances is shown in the y-axis (log scale). Distances that differ most between the two clusters (red) all involve domains at the “shoulder” region of the molecule (ANA, MG7 and MG8). (**D**) For those cross-linked pairs of residues for which mean C α -C α distances differed between clusters A and B (highlighted in red in (**C**)), the C α -C α distance for every solution (shown as crosses, purple for cluster A and green for cluster B) are plotted. The median of the distribution is represented by a red line. Cluster B show better satisfaction on residue proximities defined by cross-links.

